

Run on: May 4, 2005, 21:37:36 ; Search time 164 Seconds
 (without alignments)
 1214.522 Million cell updates/sec

Title: US-09-973-424A-66
 Perfect score: 2744
 Sequence: 1 ARGEVNLDTSTIHGDWGWL.....FSQAMEVETGKPRPRYDTRT 515

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2744	100.0	515	5 AAE23801	Aae23801 Ephrin ty
2	2744	100.0	515	8 ADF43495	Adf43495 Human eph
3	2744	100.0	515	8 ADF43467	Adf43467 Human eph
4	2744	100.0	515	8 ADJ88143	Adj88143 Human EPH
5	2744	100.0	515	8 ADJ88171	Adj88171 Human EPH
6	2744	100.0	935	8 ADF43499	Adf43499 Human eph
7	2744	100.0	935	8 ADJ88175	Adj88175 Human EPH
8	2744	100.0	992	4 AAU00691	Aau00691 Ephrin ty
9	2744	100.0	992	5 AAE23799	Aae23799 Ephrin ty
10	2744	100.0	1005	5 ABP69349	Abp69349 Human pol
11	2744	100.0	1005	8 ADF43465	Adf43465 Human eph
12	2744	100.0	1005	8 ADJ88141	Adj88141 Human EPH
13	2744	100.0	1012	4 AAE04362	Aae04362 Human kin
14	2739	99.8	935	8 ADF43497	Adf43497 Human eph
15	2739	99.8	935	8 ADJ88173	Adj88173 Human EPH
16	1708.5	62.3	539	3 AAB08667	Aab08667 A human E

17	1708.5	62.3	983	3	AAB08665	Aab08665	Amino aci
18	1708.5	62.3	983	3	AAB08666	Aab08666	A human E
19	1708.5	62.3	983	6	ABR57491	Abr57491	Human Eph
20	1708.5	62.3	983	7	AAE38583	Aae38583	Human rec
21	1708.5	62.3	983	7	ADB75273	Adb75273	Prostate
22	1708.5	62.3	983	7	ADD48947	Add48947	Human Pro
23	1708.5	62.3	983	7	ADN39284	Adn39284	Cancer/an
24	1701.5	62.0	968	5	ABP52825	Abp52825	Chicken r
25	1698.5	61.9	984	7	ADD48945	Add48945	Rat Prote
26	1697.5	61.9	983	2	AAR75711	Aar75711	Eph-relat
27	1686.5	61.5	1005	2	AAW83147	Aaw83147	Rat recep
28	1683.5	61.4	1037	6	ABR44241	Abr44241	Tyrosine
29	1682.5	61.3	983	2	AAR31466	Aar31466	HEK polyp
30	1678.5	61.2	953	5	ABP52826	Abp52826	Human rec
31	1678.5	61.2	975	5	ABP52827	Abp52827	Human Ehk
32	1678.5	61.2	991	2	AAR85090	Aar85090	EPH-like
33	1678.5	61.2	1037	5	ABG61868	Abg61868	Prostate
34	1678.5	61.2	1037	7	ADE31683	Ade31683	Human 141
35	1654	60.3	1035	5	ABG70391	Abg70391	Human Eph
36	1650	60.1	948	2	AAW83148	Aaw83148	Rat recep
37	1650	60.1	948	5	ABP52824	Abp52824	Rat recep
38	1646	60.0	1036	4	AAG67398	Aag67398	Amino aci
39	1646	60.0	1036	5	ABP52822	Abp52822	Human kin
40	1646	60.0	1036	5	ABG34081	Abg34081	Human Pro
41	1646	60.0	1036	6	AAE32033	Aae32033	Human kin
42	1646	60.0	1036	6	ADA01372	Ada01372	Human PRO
43	1646	60.0	1036	6	ADA43801	Ada43801	Human sec
44	1646	60.0	1036	6	ADA43569	Ada43569	Human sec
45	1646	60.0	1036	6	ADA01244	Ada01244	Human PRO

Run on: May 4, 2005, 21:53:26 ; Search time 43 Seconds
 (without alignments)
 894.053 Million cell updates/sec

Title: US-09-973-424A-66
 Perfect score: 2744
 Sequence: 1 ARGEVNLLDTSTIHGDWGWL.....FSQAMEVETGKPRPRYDTRT 515

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2744	100.0	1005	4	US-09-949-016-6968	Sequence 6968, Ap
2	2744	100.0	1005	4	US-09-949-016-10620	Sequence 10620, A
3	1702.5	62.0	983	1	US-08-167-919A-10	Sequence 10, Appl
4	1702.5	62.0	983	2	US-08-449-645A-21	Sequence 21, Appl
5	1702.5	62.0	983	2	US-08-702-367A-21	Sequence 21, Appl
6	1702.5	62.0	983	3	US-08-715-106-10	Sequence 10, Appl
7	1702.5	62.0	983	4	US-09-442-649-10	Sequence 10, Appl
8	1702.5	62.0	983	5	PCT-US95-04681-21	Sequence 21, Appl
9	1701.5	62.0	968	4	US-09-751-389-6	Sequence 6, Appli
10	1697.5	61.9	983	1	US-08-162-809-16	Sequence 16, Appl
11	1689	61.6	982	2	US-08-673-789-4	Sequence 4, Appli
12	1686.5	61.5	1005	2	US-08-469-537A-103	Sequence 103, App
13	1678.5	61.2	953	4	US-09-751-389-7	Sequence 7, Appli
14	1678.5	61.2	967	2	US-08-449-645A-30	Sequence 30, Appl
15	1678.5	61.2	967	2	US-08-702-367A-30	Sequence 30, Appl
16	1678.5	61.2	975	4	US-09-751-389-8	Sequence 8, Appli
17	1678.5	61.2	991	2	US-08-449-645A-13	Sequence 13, Appl
18	1678.5	61.2	991	2	US-08-702-367A-13	Sequence 13, Appl

19	1678.5	61.2	991	5	PCT-US95-04681-13	Sequence 13, Appl
20	1650	60.1	948	2	US-08-469-537A-101	Sequence 101, App
21	1650	60.1	948	4	US-09-751-389-5	Sequence 5, Appli
22	1646	60.0	1036	4	US-09-751-389-2	Sequence 2, Appli
23	1642	59.8	942	4	US-10-004-542-2	Sequence 2, Appli
24	1642	59.8	942	4	US-10-430-797-2	Sequence 2, Appli
25	1638	59.7	986	2	US-08-449-645A-15	Sequence 15, Appl
26	1638	59.7	986	2	US-08-702-367A-15	Sequence 15, Appl
27	1638	59.7	986	5	PCT-US95-04681-15	Sequence 15, Appl
28	1638	59.7	997	4	US-09-949-016-7171	Sequence 7171, Ap
29	1636	59.6	1035	4	US-09-751-389-4	Sequence 4, Appli
30	1635	59.6	998	2	US-08-449-645A-17	Sequence 17, Appl
31	1635	59.6	998	2	US-08-702-367A-17	Sequence 17, Appl
32	1635	59.6	998	4	US-09-949-016-6501	Sequence 6501, Ap
33	1635	59.6	998	5	PCT-US95-04681-17	Sequence 17, Appl
34	1635	59.6	1005	4	US-09-949-016-9901	Sequence 9901, Ap
35	1633	59.5	1104	1	US-08-222-616-36	Sequence 36, Appl
36	1633	59.5	1104	3	US-08-446-648-36	Sequence 36, Appl
37	1633	59.5	1104	4	US-09-982-610-36	Sequence 36, Appl
38	1633	59.5	1104	5	PCT-US95-04228-36	Sequence 36, Appl
39	1630	59.4	610	3	US-08-368-776A-3	Sequence 3, Appli
40	1630	59.4	610	5	PCT-US96-00419-3	Sequence 3, Appli
41	1630	59.4	626	3	US-08-368-776A-5	Sequence 5, Appli
42	1630	59.4	626	5	PCT-US96-00419-5	Sequence 5, Appli
43	1630	59.4	993	3	US-08-368-776A-11	Sequence 11, Appl
44	1630	59.4	994	3	US-08-368-776A-12	Sequence 12, Appl
45	1630	59.4	998	3	US-08-368-776A-2	Sequence 2, Appli

Run on: May 4, 2005, 21:52:16 ; Search time 42 Seconds
 (without alignments)
 1179.801 Million cell updates/sec

Title: US-09-973-424A-66
 Perfect score: 2744
 Sequence: 1 ARGEVNLLDTSTIHGDWGWL.....FSQAMEVETGKPRPRYDTRT 515

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1708.5	62.3	983	2	A38224	protein-tyrosine k
2	1701.5	62.0	983	2	B45583	receptor tyrosine
3	1698	61.9	983	2	A45583	receptor tyrosine
4	1683.5	61.4	981	2	S51604	receptor-like tyro
5	1683.5	61.4	1005	2	S49015	receptor tyrosine
6	1678.5	61.2	991	2	I78843	receptor protein-t
7	1671.5	60.9	1013	2	I50615	receptor-type prot
8	1650	60.1	948	2	S51605	receptor-like tyro
9	1638	59.7	986	2	I78844	receptor protein-t
10	1635	59.6	998	2	I58351	receptor protein-t
11	1630	59.4	605	2	JC5673	receptor tyrosine
12	1630	59.4	610	2	I48612	developmental kina
13	1630	59.4	626	2	I48614	developmental kina
14	1630	59.4	998	2	JC5672	receptor tyrosine
15	1628	59.3	985	2	I51549	receptor tyrosine
16	1618	59.0	986	2	S78059	protein-tyrosine k
17	1400	51.0	984	2	A39753	protein-tyrosine k
18	1374.5	50.1	995	2	A56599	embryo kinase 5 -
19	1363.5	49.7	970	2	I78842	receptor protein-t
20	1334	48.6	985	2	I51672	receptor tyrosine

21	1289.5	47.0	898	2	S47489	receptor tyrosine
22	1286.5	46.9	893	2	S51603	receptor-like tyro
23	1270.5	46.3	998	2	S37627	protein-tyrosine k
24	1263	46.0	993	2	I48653	mouse developmenta
25	1253.5	45.7	988	2	I50611	protein-tyrosine k
26	1251.5	45.6	952	2	I50612	protein-tyrosine k
27	1242	45.3	849	2	I50617	protein-tyrosine k
28	1190	43.4	938	2	I49071	protein kinase - m
29	1149.5	41.9	976	2	A36355	protein-tyrosine k
30	1144.5	41.7	977	2	S49004	tyrosine kinase Mp
31	1120.5	40.8	877	2	I48967	brain-specific kin
32	1084.5	39.5	975	2	I48974	receptor-protein t
33	1076	39.2	1006	2	JC5526	kinase-defective E
34	995.5	36.3	987	2	I48652	mouse developmenta
35	989.5	36.1	987	2	A54092	protein-tyrosine k
36	979.5	35.7	987	2	I48953	eph-related recept
37	934	34.0	984	1	A34076	protein-tyrosine k
38	674.5	24.6	1019	2	T13039	tyrosine kinase re
39	505.5	18.4	1122	2	T42400	Eph receptor tyros
40	360.5	13.1	919	2	T29581	hypothetical prote
41	342	12.5	612	2	S33506	protein-tyrosine k
42	245	8.9	87	2	C45583	receptor tyrosine
43	210.5	7.7	1897	1	TDHULK	leukocyte antigen-
44	206.5	7.5	1290	2	A56493	leucocyte common a
45	204.5	7.5	1825	2	C88400	protein H19M22.1 [

Run on: May 4, 2005, 21:36:36 ; Search time 135 Seconds
(without alignments)
1270.738 Million cell updates/sec

Title: US-09-973-424A-66
Perfect score: 2744
Sequence: 1 ARGEVNLLDTSTIHGDWGWL.....FSQAMEVETGKPRPRYDTRT 515

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2744	100.0	515	10	US-09-973-424A-66 Sequence 66, Appl
2	2744	100.0	515	15	US-10-449-569-4 Sequence 4, Appli
3	2744	100.0	515	15	US-10-449-569-32 Sequence 32, Appl
4	2744	100.0	935	15	US-10-449-569-36 Sequence 36, Appl

5	2744	100.0	992	10	US-09-973-424A-5	Sequence 5, Appli
6	2744	100.0	992	10	US-09-973-424A-53	Sequence 53, Appl
7	2744	100.0	992	16	US-10-691-165-5	Sequence 5, Appli
8	2744	100.0	992	16	US-10-691-165-53	Sequence 53, Appl
9	2744	100.0	1005	15	US-10-449-569-2	Sequence 2, Appli
10	2744	100.0	1012	15	US-10-168-582-3	Sequence 3, Appli
11	2739	99.8	935	15	US-10-449-569-34	Sequence 34, Appl
12	2678	97.6	991	10	US-09-973-424A-52	Sequence 52, Appl
13	2678	97.6	991	16	US-10-691-165-52	Sequence 52, Appl
14	2205	80.4	450	10	US-09-973-424A-54	Sequence 54, Appl
15	2205	80.4	450	16	US-10-691-165-54	Sequence 54, Appl
16	1708.5	62.3	666	9	US-09-771-161A-136	Sequence 136, App
17	1708.5	62.3	983	9	US-09-771-161A-227	Sequence 227, App
18	1708.5	62.3	983	14	US-10-205-823-97	Sequence 97, Appl
19	1708.5	62.3	983	14	US-10-345-680-2	Sequence 2, Appli
20	1708.5	62.3	983	15	US-10-295-027-602	Sequence 602, App
21	1708.5	62.3	983	15	US-10-029-020-59	Sequence 59, Appl
22	1701.5	62.0	968	14	US-10-412-277-6	Sequence 6, Appli
23	1683.5	61.4	1005	15	US-10-029-020-63	Sequence 63, Appl
24	1678.5	61.2	953	14	US-10-412-277-7	Sequence 7, Appli
25	1678.5	61.2	975	14	US-10-412-277-8	Sequence 8, Appli
26	1678.5	61.2	991	10	US-09-823-187-44	Sequence 44, Appl
27	1678.5	61.2	1037	14	US-10-316-124-3	Sequence 3, Appli
28	1678.5	61.2	1037	15	US-10-353-690-40	Sequence 40, Appl
29	1654	60.3	1035	15	US-10-029-020-20	Sequence 20, Appl
30	1650	60.1	948	14	US-10-412-277-5	Sequence 5, Appli
31	1648	60.1	993	10	US-09-823-187-39	Sequence 39, Appl
32	1648	60.1	993	10	US-09-823-187-41	Sequence 41, Appl
33	1646	60.0	1036	10	US-09-971-708-2	Sequence 2, Appli
34	1646	60.0	1036	14	US-10-245-752-104	Sequence 104, App
35	1646	60.0	1036	14	US-10-245-859-104	Sequence 104, App
36	1646	60.0	1036	14	US-10-245-103-104	Sequence 104, App
37	1646	60.0	1036	14	US-10-245-107-104	Sequence 104, App
38	1646	60.0	1036	14	US-10-245-143-104	Sequence 104, App
39	1646	60.0	1036	14	US-10-245-771-104	Sequence 104, App
40	1646	60.0	1036	14	US-10-245-851-104	Sequence 104, App
41	1646	60.0	1036	14	US-10-245-883-104	Sequence 104, App
42	1646	60.0	1036	14	US-10-237-535-104	Sequence 104, App
43	1646	60.0	1036	14	US-10-238-183-104	Sequence 104, App
44	1646	60.0	1036	14	US-10-238-283-104	Sequence 104, App
45	1646	60.0	1036	14	US-10-238-370-104	Sequence 104, App

Run on: May 4, 2005, 21:40:46 ; Search time 173 Seconds
 (without alignments)
 1524.398 Million cell updates/sec

Title: US-09-973-424A-66
 Perfect score: 2744
 Sequence: 1 ARGEVNLLDTSTIHGDWGWL.....FSQAMEVETGKPRPRYDTRT 515

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	2744	100.0		1005	1	EPA8_HUMAN	P29322 homo sapien
2	2678	97.6		1004	1	EPA8_MOUSE	O09127 mus musculu
3	2211	80.6		495	2	Q8IUX6	Q8iux6 homo sapien
4	2211	80.6		536	2	Q6IN80	Q6in80 homo sapien
5	1714.5	62.5		538	2	Q8C9K6	Q8c9k6 mus musculu
6	1714.5	62.5		984	2	Q8BRB1	Q8brb1 mus musculu
7	1714.5	62.5		984	2	Q8C3U1	Q8c3u1 mus musculu
8	1708.5	62.3		983	1	EPA3_HUMAN	P29320 homo sapien
9	1708.5	62.3		983	2	Q6P4R6	Q6p4r6 homo sapien
10	1701.5	62.0		983	1	EPA3_CHICK	P29318 gallus gall
11	1698.5	61.9		984	1	EPA3_RAT	O08680 rattus norv
12	1698	61.9		983	1	EPA3_MOUSE	P29319 mus musculu
13	1697.5	61.9		681	2	Q8C276	Q8c276 mus musculu
14	1683.5	61.4		1005	1	EPA5_RAT	P54757 rattus norv
15	1678.5	61.2		1037	1	EPA5_HUMAN	P54756 homo sapien
16	1671.5	60.9		1013	1	EPA5_CHICK	P54755 gallus gall
17	1650	60.1		948	1	EPA6_RAT	P54758 rattus norv
18	1649.5	60.1		969	2	Q7Z3F2	Q7z3f2 homo sapien
19	1648	60.1		993	1	EPA7_CHICK	O42422 gallus gall
20	1638	59.7		986	1	EPA4_HUMAN	P54764 homo sapien
21	1636	59.6		1035	1	EPA6_MOUSE	Q62413 mus musculu
22	1635	59.6		998	1	EPA7_HUMAN	Q15375 homo sapien

23	1631.5	59.5	986	1	EPA4_CHICK	Q07496	gallus gall
24	1631	59.4	593	2	Q8C7N2	Q8c7n2	mus musculu
25	1631	59.4	610	2	Q8CC52	Q8cc52	mus musculu
26	1631	59.4	994	2	Q8R381	Q8r381	mus musculu
27	1631	59.4	998	2	Q8BSU8	Q8bsu8	mus musculu
28	1630	59.4	998	1	EPA7_MOUSE	Q61772	mus musculu
29	1630	59.4	998	1	EPA7_RAT	P54759	rattus norv
30	1628	59.3	985	1	EP4B_XENLA	Q91694	xenopus lae
31	1628	59.3	986	2	Q7ZYM7	Q7zym7	xenopus lae
32	1624	59.2	986	1	EP4A_XENLA	Q91845	xenopus lae
33	1623	59.1	986	2	Q80VZ2	Q80vz2	mus musculu
34	1618	59.0	986	1	EPA4_MOUSE	Q03137	mus musculu
35	1549.5	56.5	927	2	Q99KA8	Q99ka8	mus musculu
36	1524.5	55.6	976	2	Q90ZN9	Q90zn9	brachydanio
37	1522	55.5	880	2	O73879	O73879	brachydanio
38	1508.5	55.0	981	1	EPA3_BRARE	O13146	brachydanio
39	1400	51.0	984	1	EPB1_RAT	P09759	rattus norv
40	1398	50.9	984	1	EPB1_HUMAN	P54762	homo sapien
41	1395	50.8	943	2	Q8CBE2	Q8cbe2	mus musculu
42	1395	50.8	984	2	Q8CBF3	Q8cbf3	mus musculu
43	1387	50.5	984	2	Q6PG23	Q6pg23	mus musculu
44	1379.5	50.3	994	1	EPB2_MOUSE	P54763	mus musculu
45	1379.5	50.3	1021	2	Q6GTQ7	Q6gtq7	mus musculu